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ctattgacag ctttaggcat atgtatgtgt ttggagactt caaagatgta 1150

ttaattcctg gaaaactcaa gcaattcgta tttgacttac attctggaaa 1200

actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250

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gctttaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400

cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450

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<211> 406
<212> PRT
<213> Homo sapiens

<400> 309

Met	His	Pro	Ala	Val	Phe	Leu	Ser	Leu	Pro	Asp	Leu	Arg	Cys	Ser	
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Leu	Leu	Leu	Leu	Val	Thr	Trp	Val	Phe	Thr	Pro	Val	Thr	Thr	Glu	
				20				25						30	
Ile	Thr	Ser	Leu	Ala	Thr	Glu	Asn	Ile	Asp	Glu	Ile	Leu	Asn	Asn	
				35				40						45	
Ala	Asp	Val	Ala	Leu	Val	Asn	Phe	Tyr	Ala	Asp	Trp	Cys	Arg	Phe	
				50				55						60	
Ser	Gln	Met	Leu	His	Pro	Ile	Phe	Glu	Glu	Ala	Ser	Asp	Val	Ile	
				65				70						75	
Lys	Glu	Glu	Phe	Pro	Asn	Glu	Asn	Gln	Val	Val	Phe	Ala	Arg	Val	
				80				85						90	
Asp	Cys	Asp	Gln	His	Ser	Asp	Ile	Ala	Gln	Arg	Tyr	Arg	Ile	Ser	
				95				100						105	
Lys	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Arg	Asn	Gly	Met	Met	Met	Lys	
				110				115						120	
Arg	Glu	Tyr	Arg	Gly	Gln	Arg	Ser	Val	Lys	Ala	Leu	Ala	Asp	Tyr	
				125				130						135	
Ile	Arg	Gln	Gln	Lys	Ser	Asp	Pro	Ile	Gln	Glu	Ile	Arg	Asp	Leu	
				140				145						150	
Ala	Glu	Ile	Thr	Thr	Leu	Asp	Arg	Ser	Lys	Arg	Asn	Ile	Ile	Gly	
				155				160						165	

Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg
170 175 180

Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe
185 190 195

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile
200 205 210

Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly
215 220 225

Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys
230 235 240

Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu
245 250 255

Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys
260 265 270

Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg
275 280 285

Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp
290 295 300

Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro
305 310 315

Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr
320 325 330

Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys
335 340 345

Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe
350 355 360

His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala
365 370 375

Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu
380 385 390

Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu
395 400 405

Leu

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<211> 182
<212> DNA
<213> Homo sapiens

<220>
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<222> 36, 48
<223> unknown base

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caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150

ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311
<211> 598
<212> DNA
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<220>
<221> unsure
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396
<223> unknown base

<400> 311
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cggagcccag ccctttccta acccaaccca acctagcccn gtcccagccg 150

ccagcgcctg tccctgtcnc gganccccagc gtnaccatgc atcctgccgt 200

cttcctatcc ttacccgacc tcagatgctc ccttctgctc ctggtaactt 250

gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300

atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350

tgactggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400

ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450

agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 500

caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550

aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
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